
FACSIMILE MESSAGE - PLEASE DELIVER PROMPTLY

November 11, 2002

TO: Examiner Bridget Bunner
Group 1647
(703) 308-7148FROM Lin Sun-Hoffman
Celera Genomics Corp.
(240) 453-3628FAX NO: (703) 308-4242# OF PAGES (incl. cover): 8

Re: U.S. Serial No. 09/776,705, filed Feb. 6, 2001
Entitled "ISOLATED HUMAN TRANSPORTER, NUCLEIC ACID
MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, AND
USES THEREOF"

A Preliminary Amendment (Restriction Election) and a Statement Regarding Duty of Disclosure and a request of two-month extension of time in the above-identified application follows. No fee is due for this filing.

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: GUEGLER et al.

Art Unit: 1647

Serial No. 09/776,705

Examiner: B. Bunner

Filed: February 6, 2001

Atty. Docket: CL001010

For: ISOLATED HUMAN TRANSPORTER
PROTEINS, NUCLEIC ACID MOLECULES
ENCODING HUMAN TRANSPORTER
PROTEINS, AND USES THEREOF

**Statement Regarding Duty Of Disclose Information Material To Patentability
Under 37 CFR 1.56 (a) and (b)**

Honorable Commissioner of
Patents and Trademarks
Washington, D.C. 20231

By Facsimile

Sir:

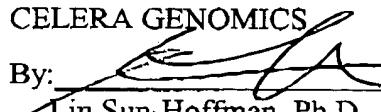
This statement is to inform the United States of Patent and Trademark Office that Applicants and their representative have made a good faith effort in searching prior art relating to this invention.

No prior art material to patentability of the present invention has been found. The closest information associated with the invention is disclosed in Figures 1 and 2 in the top BLAST search results. However, this information, by itself or in combination with other information, does not constitute a *prima facie* case of unpatentability of any of the pending claims. Thus, it does not defeat the novelty of the present invention and the actual underlying references for the top BLAST hits are not being provided.

Respectfully submitted,

CELERA GENOMICS

By:


Lin Sun-Hoffman, Ph.D., Reg No. 47,983Date: Nov. 11, 2001

Celera Genomics Corporation
45 West Gude Drive, C2-4#20
Rockville, MD 20850
Tel: 240-453-3628, Fax: 240-453-3084

BLAST SEARCH RESULT AGAINST GENESEQ AND NCBI DATABASE CL001010

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 1010
(547 letters)

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Searching.....done

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Query: 541 PPNSKHH 547
PPNSKHH
Sbjct: 540 PPNSKHH 546

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jingui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 1010
(547 letters)

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119,338 sequences; 19,610,776 total letters

Searching.....done

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Length = 547

Score = 1084 bits (2774). Expect = 0.0
Identities = 543/547 (99%), Positives = 544/547 (99%)

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Query: 61 KKLADYADEHHPGTTSGMSSFNLSNAIMGSIGLGLSYAMAYTGVILFIIMLLAVAILSL 120
KKLADYADEHHPGTTSGMSSFNLSNAIMGSIGLGLSYAMA TG+ILFIIMLLAVAILSL
Sbjct: 61 KKLADYADEHHPGTTSGMSSFNLSNAIMGSIGLGLSYAMANTGHILFIIMLLAVAILSL 120

Query: 121 YSVHLLLKTAKEGGSLIYEKLGEKAFGWPKGIGAFVSIQMNINGAMSSYLFIIKYELPEV 180
YSVHLLLKTAKEGGSLIYEKLGEKAFGWPKGIGAFVSIQMNINGAMSSYLFIIKYELPEV
Sbjct: 121 YSVHLLLKTAKEGGSLIYEKLGEKAFGWPKGIGAFVSIQMNINGAMSSYLFIIKYELPEV 180

Query: 181 IRAFMGLEENTGEWYLNGNYLIIFVSVGIIPLSLLKNLGYLGTYSGFSLTCMVFFVSVV 240
IRAFMGLEENTGEWYLNGNYLIIFVSVGIIPLSLLKNLGYLGTYSGFSLTCMVFFVSVV
Sbjct: 181 IRAFMGLEENTGEWYLNGNYLIIFVSVGIIPLSLLKNLGYLGTYSGFSLTCMVFFVSVV 240

Query: 241 IYKKFQIPCPPLPVLDHSVGNLNFNNLTPMHVVMLPNNSESSDVNFMDYTHRNPAGLDEN 300
IYKKFQIPCPPLPVLDHSVGNLNFNNLTPMHVVMLPNNSESSDVNFMDYTHRNPAGLDEN
Sbjct: 241 IYKKFQIPCPPLPVLDHSVGNLNFNNLTPMHVVMLPNNSESSDVNFMDYTHRNPAGLDEN 300

Query: 301 QAKGSLHDMSGVEYEAHSDDKCEPKYFVNSRTAYAIPILVFAFVCHPEVLPYSELKDRS 360
QAKGSLHDMSGVEYEAHSDDKCEPKYFVNSRTAYAIPILVFAFVCHPEVLPYSELKDRS
Sbjct: 301 QAKGSLHDMSGVEYEAHSDDKCEPKYFVNSRTAYAIPILVFAFVCHPEVLPYSELKDRS 360

Query: 361 RRKMQTVSNSITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLIDPLLMVRALVL 420
RRKMQTVSNSITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLIDPLLMVRALVL
Sbjct: 361 RRKMQTVSNSITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLIDPLLMVRALVL 420

Query: 421 VAVTQTVPIVLFPIRTSVITLLFPKRPFWSIRHFLIAAVLIALNNVLVILVPTIKYIFGF 480
VAVTQTVPIVLFPIRTSVITLLFPKRPFWSIRHFLIAAVLIALNNVLVILVPTIKYIFGF
Sbjct: 421 VAVTQTVPIVLFPIRTSVITLLFPKRPFWSIRHFLIAAVLIALNNVLVILVPTIKYIFGF 480

Query: 481 IGASSATMLIFILPAVFYLKLVKETFRSPQKVGVGALIFLVVGIFFMIGSMALIIDWIYD 540
IGASSATMLIFILPAVFYLKLVKETFRSPQKVGVGALIFLVVGIFFMIGSMALIIDWIYD
Sbjct: 481 IGASSATMLIFILPAVFYLKLVKETFRSPQKVGVGALIFLVVGIFFMIGSMALIIDWIYD 540

Query: 541 PPNSKHH 547
PPNSKHH
Sbjct: 541 PPNSKHH 547

>CRA|225000041339589 /altid=gi|19169919 /def=emb|CAD26771.1| unnamed
protein product [Homo sapiens] /org=Homo sapiens
/taxon=9606 /div=PRI /dataset=pataa /length=487
Length = 487

Score = 476 bits (1212), Expect = e-134
Identities = 258/543 (47%), Positives = 350/543 (63%), Gaps = 67/543 (12%)

Query: 5 ELRNVNIEPDDDESSSGESAPDSYIRGNSEKAAMSSQFANEDTESQKFLTNGFLGKKLA 64
EL+N+ + P+D++ S+S ++ N + ++S+F+ D ES++ LTN L KKK
Sbjct: 12 ELQNMTV-PEDDNISNDS--NDFTEVENQ--INSKFIS-DRESRRSLTNSHLEK-- 62

Query: 65 DYADEHHPGTTSGMSSFNLSNAIMGSIGLGLSYAMAYTGVILFIIMLLAVAILS LYSVH 124
DE+HPGTTSGMSSFNLSNAIMGSIGLGLSYAMA TG+LF++L +V +LS+YS++
Sbjct: 63 --CDEYHPGTTSGMSSFNLSNAIVGSGILGLSYAMANTGIALFMVLLTSVTLLSIYSIN 120

Query: 125 LLLKTAKEGGSLIYEKLGEKAFGWPKGIGAFVSIQMNINGAMSSYLFIIKYELPEVIRAF 184
LLL +KE G ++YEKLGE+ FG GK F + ++QN GAM SYLFI+K ELP I+

Sbjct: 121 LLLCSKETGCMVYEKLGEGVFGTTGKFVIFGATSLQNTGAMLSYLFIVKNELPSAIKEL 180

Query: 185 MGLEENTGEWYLNNGNYLIIHVSVGIIILPLSLLKNLGGLGTYSGFSLTCMVFFSVVIYKK 244
MG EE WY++G L++ V+ GIILPL LLKNLGLGTYSGFSL+CMVFF+ VVIYKK

Sbjct: 181 MGKEETFSAWYVDGRVLVVIVTFGIIPLC'LLKNLGGLGTYSGFSLSCMVFFLIVVIYKK 240

Query: 245 FQIPCPLPVLDHSVGNLNFNNLPMHVMLPNSESDVNFMMDYTHRNPAGLDENQAKG 304
FQIPC +P L+ ++ NS ++D

Sbjct: 241 FQIPCIVPELNSTIS-----ANSTNADT----- 263

Query: 305 SLHDSGVVEYEAHSDDKCEPKYFVFNRSRTAYAIPILVFAFVCHPEVLPIYSELKDRSRKM 364
C PKY FNS+T YA+P + FAFVCHP VLPIYSELKDRS++KM

Sbjct: 264 -----CTPKYVTNSKTVYALPTIAFAFVCHPSVLPIYSELKDRSQKKM 307

Query: 365 QTWSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLIDIPLLMVRЛАLVAVT 424
Q VSNIS M VMY L A+FGYLTFY V+ +LLH Y DI+L VRLAV+VAV

Sbjct: 308 QMVSNISSFFAMFVMYFLTAIFGYLTFYDNVQSLLLHKYQS--KDDILILTВRLAVIVAVI 365

Query: 425 QTVPIVLFPIRTSVITLLFPKRPFWSIRHFLIAAVLIALNNVLVILVPTIKYIFGFIGAS 484
TVP++ F+R+S+ L K F+ RH ++ +L+ + N+LVI+P++K IFG +G +

Sbjct: 366 LTVPVLFFTVRSSLFELA-KKTKFNLCRHTVVTCILLVVINLLVIFIPSMKDIFGVVGVT 424

Query: 485 SATMLIFILPAVFYLKLVKKETFRSPQKVGVGALIFLVVGIFFMIGSMALIIDWIYDPPNS 544
SA MLIFILP+ YLK+ ++ + Q++ A +FL +G+ F + S+ L+IDW +

Sbjct: 425 SANMLIFILPSSLYLKITDQDGDKGTQRIWAALFLGLGVLFSLVSIPLVIYDWACSSSD 484

Query: 545 KHH 547
+ H
Sbjct: 485 EGH 487